

IN THE CLAIMS:

Cancel claims 13-27, 29, and 30 without prejudice or disclaimer.

Please amend the claims and add new claims 45-50 as shown below:

Claims 1-4 (cancelled)

Claim 5 (previously presented): An isolated polynucleotide comprising the nucleotide sequence of SEQ ID No. 1.

Claim 6-8 (cancelled)

Claim 9 (previously presented): An isolated polynucleotide sequence which encodes a polypeptide comprising the amino acid sequence of SEQ ID No. 2.

Claims 10 and 11 (cancelled)

Claim 12 (original): An Escherichia coli strain DH5amcr/pEC-XK99EsigMaleX deposited as DSM 14409.

Claims 13-30 (canceled)

Claim 31 (previously presented): An isolated polynucleotide comprising nucleotides 236 to 907 of SEQ ID NO: 1.

Claim 32 (currently amended): An isolated polynucleotide comprising the nucleotide sequence of the complete complement of the polynucleotide of claim 31 nucleotides 236 to 907 of SEQ ID NO: 1.

Claim 33 (currently amended): An isolated polynucleotide comprising the nucleotide sequence of the complete complement of the polynucleotide of claim 5 SEQ ID NO: 1.

Claim 34 (currently amended) A vector comprising the polynucleotide of any one of claims 5, 9, or 31, 32 or to 33.

Claim 35 (previously presented): The vector according to claim 34, wherein said vector is pEC-XK99sigMa1ex as deposited in DSM14409.

Claim 36 (previously presented): A bacterium comprising the vector of claim 34, wherein said bacterium is an E. coli or a coryneform bacterium.

Claim 37 (currently amended): A bacterium comprising the polynucleotide of any one of claims 5, 9, or 31, 32 or to 33, wherein said bacterium is an E. coli or a coryneform bacterium.

Claim 38 (previously presented): An isolated polynucleotide primer or probe consisting of a DNA or RNA fragment, wherein said fragment consists of at least 30 consecutive nucleotides from SEQ ID NO: 1.

Claim 39 (previously presented): An isolated polynucleotide primer or probe consisting of a DNA or RNA fragment, wherein said fragment consists of at least 40 consecutive nucleotides from SEQ ID NO: 1.

Claims 40-43 (canceled)

Claim 44 (previously presented): A recombinant *Corynebacterium glutamicum* comprising an overexpressed polynucleotide encoding a polypeptide having the amino acid sequence of SEQ ID NO:2, wherein overexpression is achieved by increasing the copy number of said polynucleotide or by operably linking a promoter to said polynucleotide.

Claim 45 (new): A method for the production of L-amino acids using coryneform bacteris, comprising:

a) fermenting coryneform bacteria comprising an overexpressed sigM polynucleotide wherein said polynucleotide comprises a nucleotide sequence according to any one of claims 5, 9, 31 or 33, wherein said overexpression is achieved by increasing the copy number of said polynucleotide or by operably linking said polynucleotide to a promoter.

Claim 46 (new): The method according to claim 45, further comprising:

b) isolating the L-amino acids.

Claim 47 (new): The method as claimed in claim 45, wherein the L- amino acid produced is L-lysine.

Claim 48 (new): The method as claimed in claim 45, wherein the bacteria comprise, at the same time, one or more endogenous *Corynebacterium glutamicum* genes which are overexpressed, wherein the one or more genes is/are selected from the group consisting of:

- the gene which encodes dihydridipicolinate synthase,
- the gene which encodes glyceraldehyde-3-phosphate dehydrogenase,
- the gene which encodes triose phosphate isomerase,
- the gene which encodes 3-phosphoglycerate kinase,
- the gene which encodes glucose-6-phosphate dehydrogenase,
- the gene which encodes pyruvate carboxylase,
- the gene which encodes malate quinone oxidoreductase,
- the gene which encodes an aspartate kinase,
- the gene which encodes a protein which exports lysine,
- the gene which encodes homoserine dehydrogenase,
- the gene which encodes threonine dehydratase,
- the gene which encodes acetohydroxy acid synthase,
- the gene which encodes dihydroxy acid dehydratase, and
- the gene which encodes the Zwa1 protein.

Claim 49 (new): The method as claimed in claim 45, wherein the bacteria comprise, at the same time, one or more endogenous *Corynebacterium glutamicum* genes which are eliminated, wherein said one or more genes is/are selected from the group consisting of:

- the gene which encodes phosphoenol pyruvate carboxykinase,
- the gene which encodes glucose-6-phosphate isomerase,

the gene which encodes pyruvate oxidase, and
the gene which encodes the Zwa2 protein.

Claim 50 (new): The method according to claim 45, wherein the bacteria are
Corynebacterium glutamicum.